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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/987,455

DATE: 01/15/2002

TIME: 11:56:43

Input Set : A:\Seqlis-1

Output Set: N:\CRF3\01152002\I987455.raw

4 <110> APPLICANT: Aranya Manosroi
 5 Jiradej Manosroi
 6 Chatchai Tayapiwatana
 7 Friedrich Goetz
 8 Rolf-Guenther Werner
 10 <120> TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
 11 DNA-Derived tPA or K2S Molecules
 13 <130> FILE REFERENCE: 0652.2190001
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/987,455
 C--> 15 <141> CURRENT FILING DATE: 2001-11-14
 15 <150> PRIOR APPLICATION NUMBER: 60/268,574
 16 <151> PRIOR FILING DATE: 2001-02-15
 18 <150> PRIOR APPLICATION NUMBER: GB 0027779.8
 19 <151> PRIOR FILING DATE: 2000-11-14
 21 <160> NUMBER OF SEQ ID NOS: 25
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 18
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: coding
 32 sequence of N-terminal part of K2S protein
 34 <400> SEQUENCE: 1
 35 tctgaggaa acagtgac 18
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 1128
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Artificial Sequence
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 44 <223> OTHER INFORMATION: Description of Artificial Sequence: coding
 45 sequence for OmpA-K2S fusion protein
 47 <400> SEQUENCE: 2
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 49 gccgcctctg agggaaacag tgactgctac tttggaaatg ggtcagccctt ccgtggc 120
 50 cacagcctca ccgagtcggg tgcctcctgc ctcccgtgga attccatgtat cctgataggc 180
 51 aaggtttaca cagcacagaa ccccaagtggc caggcactgg gcctggccaa acataattac 240
 52 tgccggaatc ctgatggggta tgccaaagccc tggtgccacg tgctgaagaa ccgcaggctg 300
 53 acgtgggagt actgtgatgt gcccctctgc tccacctgc gcctgagaca gtacagccag 360
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 55 gccatctttg ccaagcacag gaggtcgccc ggagagcggt tcctgtcg 480
 56 atcagcttct gctggattct ctctggcc cactgcttcc aggagaggtt tccggcc 540
 57 cacctgacgg tggatcttggg cagaacatac cgggtggcc tggcgagga ggagcagaaa 600
 58 tttgaagtcg aaaaatacat tggccataag gaattcgatg atgacactta cgacaatgac 660
 59 attgcgctgc tgcagctgaa atcggattcg tcccgctgtg cccaggagag cagcgtggc 720
 60 cgactgtgt gcctcccccc ggcggacctg cagctgccgg actggacgga gtgtgagctc 780
 61 tccggctacg gcaagcatga ggccttgc ctttcttatt cggagcggct 840

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62 catgtcagac tgtaccatc cagccgctgc acatcacaac atttacttaa cagaacagtc 900
63 accgacaaca tgctgtgtgc tgagacact cggagccggc ggcggccagc aaacttgcac 960
64 gacgcctgcc agggcgattc gggaggcccc ctgggtgtgc tgaacgatgg ccgcattgact 1020
65 ttgggtggca tcatcagctg gggcctggc tggacaga aggatgtccc ggggtgttac 1080
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69 <210> SEQ ID NO: 3
70 <211> LENGTH: 66
71 <212> TYPE: DNA
72 <213> ORGANISM: Escherichia coli
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76 gcggcc 66
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81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence: coding
86 sequence for K2S protein
88 <400> SEQUENCE: 4
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90 ctcaccgagt cgggtgcctc ctgcctcccg tgaaattcca tgatcctgtt aggcaaggaa 120
91 tacacagcac agaaccggc tggccaggca ctggggctgg gcaaacataa ttactgcccgg 180
92 aatccctgatg gggatgccaa gcccgtgtgc cacgtgtga agaaccgcag gctgacgtgg 240
93 gagtaactgtg atgtgcctc ctgtccacc tgccgtgtga gacagtacag ccagcctcag 300
94 tttcgcatca aaggagggtt cttcgccgac atgcctccc accccctggca ggctgcccattc 360
95 tttgccaaggc acaggaggc gcccggagag cgggttctgt gggggggcat actcatcagc 420
96 tcctgcttgc ttctctctgc cggccactgc ttccaggaga gttttccggcc ccaccacctg 480
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98 gtcgaaaaat acattgtcca taaggaaattt gatgtgaca cttacgacaa tgacatttgc 600
99 ctgctgcagc taaaatcggaa ttctcccgc tggcccagg agagcagcgt ggtccgcact 660
100 gtgtgccttc cccggcggaa cctgcagctg cggactggaa cggagtgtga gctctccggc 720
101 tacggcaagc atgaggcctt gtctccttgc tattcggagc ggctgaagga ggctcatgtc 780
102 agactgtacc catccagccg ctgcacatca caacatttac ttaacagaac agtcacccgac 840
103 aacatgctgt gtgctggaga cactcggagc ggcggggcccc aggcaactt gcacgacgac 900
104 tgccaggccg attcggggagg cccctgggtt tgcgtgaacg atggcccat gactttgggt 960
105 ggcacatcatca gctggggcct gggctgttgc cagaaggatg tcccggtgt gtacacaaag 1020
106 gttaccaact accttagactg gattcgtgac aacatgcgac cgtga 1065
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110 <211> LENGTH: 1128
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: coding
116 sequence for OmpA-K2S fusion protein
118 <400> SEQUENCE: 5
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120 gcggccctgt agggaaacag tgactgtac tttggaaatg ggtcagccta ccgtggcact 120
121 cacagcctca ccgagtcggg tgcctctgc ctccctgttgc attccatgtt cctgataggc 180

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122 aaggtttaca cagcacagaa ccccagtgcc caggcactgg gcctgggcaa acataattac 240
 123 tgccggaatc ctgatgggaa tgccaagccc tggtgccacg tgctgaagaa ccgcaggctg 300
 124 acgtgggagt actgtatgt gccccttc tccacacctg gcctgagaca gtacagccag 360
 125 cctcgtttc gcatcaaagg agggctcttc gcccacatcg cctccaccc ctgcaggct 420
 126 gccatctttg ccaagcacag gaggtcgccc ggagagcggt tcctgtgcgg gggcataactc 480
 127 atcagctcct gctggattct ctctgccc cactgcttcc aggagaggtt tccgccccac 540
 128 cacctgacgg ttagtcttggg cagaacatac cgggtggtcc ctggcgagga ggagcagaaa 600
 129 tttgaagtcg aaaaatacat tggccataaag gaattcgatg atgacactt cgacaatgac 660
 130 attgcgctgc tgcagctgaa atcggattcg tcccgcgtg cccaggagag cagcgtggtc 720
 131 cgcactgtgt gccttccccc ggcggacctg cagctgccc actggacgga gtgtgagctc 780
 132 tccggctacg gcaagcatga ggccttgc ccttctatt cggagcggct gaaggaggct 840
 133 catgtcagac tgcgtccatc cagccgctgc acatcacaac atttacttaa cagaacagtc 900
 134 accgacaaca tgcgtgtgc tggagacact cggagcggcg ggccccaggc aaacttgcac 960
 135 gacgcctgcc agggcgattc gggaggcccc ctgggtgtgc tgaacgtgg ccgcattact 1020
 136 ttgggtggca tcatcagctg gggcctggc tggacaga agatgtccc ggggtgtac 1080
 137 acaaaggta ccaactacat agactggatt cgtgacaaca tgcgaccc 1128
 140 <210> SEQ ID NO: 6
 141 <211> LENGTH: 66
 142 <212> TYPE: DNA
 143 <213> ORGANISM: Escherichia coli
 145 <400> SEQUENCE: 6
 146 atgaaaaaga cagctatcgc gattgcagtgc gcaactggctg gtttcgtac cgtggcccg 60
 147 gcggcc 66
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 151 <211> LENGTH: 1065
 152 <212> TYPE: DNA
 153 <213> ORGANISM: Artificial Sequence
 155 <220> FEATURE:
 156 <223> OTHER INFORMATION: Description of Artificial Sequence: coding
 sequence for K2S protein
 157 <400> SEQUENCE: 7
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 161 ctcaccgagt cgggtgcctc ctgcctcccg tggaaattcca tgatcctgtat aggcaagggtt 120
 162 tacacacgac agaaccggcag tggccaggca ctgggcctgg gcaaacataa ttactgccc 180
 163 aatcctgtat gggatgcac gcccctggc acgtgtcga agaaccgcag gctgacgtgg 240
 164 gagttactgt atgtgcctc ctgcctccacc tgcggcctga gacagtacag ccagcctcag 300
 165 tttcgatca aaggagggtt ctgcggcgtc atgcctccc acccctggca ggctgcccattc 360
 166 tttgccaaggc acaggagggtc gcccggagag cggttcctgt gccccggcat actcatcagc 420
 167 tcctgtggc ttctctctgc cggccactgc ttccaggaga ggtttccgccc ccaccacctg 480
 168 acgggtatct tggcagaac ataccgggtt gtcctggcg aggaggagca gaaatttggaa 540
 169 gtcggaaaat acattgttca taaggaattc gatgtgaca ttacgacaa tgacattgcg 600
 170 ctgtgcagc tgaaatcgga ttgcgtcccg tggccagg agagcagcgt ggtccgcact 660
 171 gtgtgccttc ccccgccgaa cctgcagctg ccggactggaa cggagtgta gctctccggc 720
 172 tacggcaaggc atgaggcctt gtctccttcc tattggagc ggctgaagga ggctcatgtc 780
 173 agactgtacc catccagccg ctgcacatca caacattac ttaacagaac agtacaccgac 840
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 175 tgccaggggcg attcggggagg cccctgggtt tggctgtacg atggccgcat gactttgggt 960
 176 ggcacatca gctggggcct gggctgtggc cagaaggatg tcccggtgt gtacacaaaag 1020
 177 gttaccaact accttagactg gattcgtgac aacatgcgac cgtga 1065

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180 <210> SEQ ID NO: 8
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182 <212> TYPE: PRT
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: OmpA-K2S
187 fusion protein
189 <400> SEQUENCE: 8
190 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
191 1 5 10 15
193 Thr Val Ala Gln Ala Ala Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly
194 20 25 30
196 Asn Gly Ser Ala Tyr Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala
197 35 40 45
199 Ser Cys Leu Pro Trp Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr
200 50 55 60
202 Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr
203 65 70 75 80
205 Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys
206 85 90 95
208 Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr
209 100 105 110
211 Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly
212 115 120 125
214 Leu Phe Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala
215 130 135 140
217 Lys His Arg Arg Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu
218 145 150 155 160
220 Ile Ser Ser Cys Trp Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg
221 165 170 175
223 Phe Pro Pro His His Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val
224 180 185 190
226 Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val
227 195 200 205
229 His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu
230 210 215 220
232 Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val
233 225 230 235 240
235 Arg Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr
236 245 250 255
238 Glu Cys Glu Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe
239 260 265 270
241 Tyr Ser Glu Arg Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser
242 275 280 285
244 Arg Cys Thr Ser Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn Met
245 290 295 300
247 Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His
248 305 310 315 320
250 Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp

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251 325 330 335
253 Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
254 340 345 350
256 Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp
257 355 360 365
259 Trp Ile Arg Asp Asn Met Arg Pro Gly
260 370 375
263 <210> SEQ ID NO: 9
264 <211> LENGTH: 4
265 <212> TYPE: PRT
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
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272 <400> SEQUENCE: 9
273 Ser Glu Gly Asn
274 1
277 <210> SEQ ID NO: 10
278 <211> LENGTH: 6
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
284 sequence
286 <400> SEQUENCE: 10
287 Ser Glu Gly Asn Ser Asp
288 1 5
291 <210> SEQ ID NO: 11
292 <211> LENGTH: 354
293 <212> TYPE: PRT
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: K2S 174-527
299 <400> SEQUENCE: 11
300 Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
301 1 5 10 15
303 Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
304 20 25 30
306 Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
307 35 40 45
309 Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
310 50 55 60
312 Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
313 65 70 75 80
315 Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
316 85 90 95
318 Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
319 100 105 110
321 Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro

VERIFICATION SUMMARY
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date